

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising:
 - (a) a first nucleotide sequence encoding a first polypeptide comprising at least 50 amino acids, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:10 have at least 95% identity based on the Clustal alignment method,
 - (b) a second nucleotide sequence encoding a second polypeptide comprising at least 95 amino acids, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 90% identity based on the Clustal alignment method,
 - (c) a third nucleotide sequence encoding a third polypeptide comprising at least 100 amino acids, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 70% identity based on the Clustal alignment method,
 - (d) a fourth nucleotide sequence encoding a fourth polypeptide comprising at least 100 amino acids, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 80% identity based on the Clustal alignment method,
 - (e) a fifth nucleotide sequence encoding a fifth polypeptide comprising at least 250 amino acids, wherein the amino acid sequence of the fifth polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 80% identity based on the Clustal alignment method,
 - (f) a sixth nucleotide sequence encoding a sixth polypeptide comprising at least 400 amino acids, wherein the amino acid sequence of the sixth polypeptide and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 85% identity based on the Clustal alignment method,
 - (g) a seventh nucleotide sequence encoding a seventh polypeptide comprising at least 400 amino acids, wherein the amino acid sequence of the seventh polypeptide and the amino acid sequence of SEQ ID NO:16 have at least 90% identity based on the Clustal alignment method, or
 - (h) the complement of the first, second, third, fourth, fifth, sixth, or seventh nucleotide sequence, wherein the complement and the first, second, third, fourth, fifth, sixth, or seventh nucleotide sequence contain the same number of nucleotides and are 100% complementary.
2. The polynucleotide of Claim 1, wherein the first and second polypeptides comprise at least 100 amino acids.

3. The polynucleotide of Claim 1, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 80% identity based on the Clustal alignment method.

4. The polynucleotide of Claim 1, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 85% identity based on the Clustal alignment method, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 85% identity based on the Clustal alignment method, and wherein the amino acid sequence of the fifth polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 85% identity based on the Clustal alignment method.

5. The polynucleotide of Claim 1, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 90% identity based on the Clustal alignment method, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 90% identity based on the Clustal alignment method, wherein the amino acid sequence of the fifth polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 90% identity based on the Clustal alignment method, and wherein the amino acid sequence of the sixth polypeptide and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 90% identity based on the Clustal alignment method.

6. The polynucleotide of Claim 1, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the fifth polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the sixth polypeptide and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 95% identity based on the Clustal alignment method, and wherein the amino acid sequence of the seventh polypeptide and the amino acid sequence of SEQ ID NO:16 have at least 95% identity based on the Clustal alignment method.

7. The isolated polynucleotide of Claim 1, wherein the first polypeptide comprises the amino acid sequence of SEQ ID NO:10, wherein the second polypeptide comprises the amino acid sequence of SEQ ID NO:2, wherein the third polypeptide comprises the amino acid sequence of SEQ ID NO:4, wherein the fourth polypeptide comprises the amino acid sequence of SEQ ID NO:14, wherein the fifth polypeptide comprises the amino acid

5 (e) a fifth amino acid sequence comprising at least 250 amino acids, wherein the fifth amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 80% identity based on the Clustal alignment method,

10 (f) a sixth amino acid sequence comprising at least 400 amino acids, wherein the sixth amino acid sequence and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 85% identity based on the Clustal alignment method, or

15 (g) a seventh amino acid sequence comprising at least 400 amino acids, wherein the seventh amino acid sequence and the amino acid sequence of SEQ ID NO:16 have at least 90% identity based on the Clustal alignment method.

20 16. The polypeptide of Claim 15, wherein the first and second amino acid sequences comprise at least 100 amino acids.

25 17. The polypeptide of Claim 15, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:4 have at least 80% identity based on the Clustal alignment method.

30 18. The polypeptide of Claim 15, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:4 have at least 85% identity based on the Clustal alignment method, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 85% identity based on the Clustal alignment method, and wherein the fifth amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 85% identity based on the Clustal alignment method.

35 19. The polypeptide of Claim 15, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:4 have at least 90% identity based on the Clustal alignment method, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 90% identity based on the Clustal alignment method, wherein the fifth amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 90% identity based on the Clustal alignment method, and wherein the sixth amino acid sequence and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 90% identity based on the Clustal alignment method.

40 20. The polypeptide of Claim 15, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:2 have at least 95% identity based on the Clustal alignment method, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:4 have at least 95% identity based on the Clustal alignment method, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 95% identity based on the Clustal alignment method, wherein the fifth amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 95% identity based on the Clustal alignment method, wherein the sixth amino acid sequence and the amino acid

sequence of SEQ ID NO:12, wherein the sixth polypeptide comprises the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8, and wherein the seventh polypeptide comprises the amino acid sequence of SEQ ID NO:16.

8. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:9, wherein the second nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:1, wherein the third nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:3, wherein the fourth nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:13, wherein the fifth nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:11, wherein the sixth nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:5 or SEQ ID NO:7, and wherein the seventh nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:15.

9. The isolated polynucleotide of Claim 1, wherein the first, second, third, fourth, fifth, sixth, and seventh polypeptides are aspartate kinases.

10. A chimeric gene comprising the polynucleotide of any of Claims 1-9 operably linked to a regulatory sequence.

11. A vector comprising the polynucleotide of any of Claims 1-9.

12. An isolated polynucleotide fragment comprising a nucleotide sequence comprised by the polynucleotide of any of Claims 1-9, wherein the nucleotide sequence contains at least 30 nucleotides.

13. The fragment of Claim 12, wherein the nucleotide sequence contains at least 40 nucleotides.

14. The fragment of Claim 12, wherein the nucleotide sequence contains at least 60 nucleotides.

15. An isolated polypeptide comprising:

- (a) a first amino acid sequence comprising at least 50 amino acids, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:10 have at least 95% identity based on the Clustal alignment method,
- (b) a second amino acid sequence comprising at least 95 amino acids, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:2 have at least 90% identity based on the Clustal alignment method,
- (c) a third amino acid sequence comprising at least 100 amino acids, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:4 have at least 70% identity based on the Clustal alignment method,
- (d) a fourth amino acid sequence comprising at least 100 amino acids, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 80% identity based on the Clustal alignment method,

sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 95% identity based on the Clustal alignment method, and wherein the seventh amino acid sequence and the amino acid sequence of SEQ ID NO:16 have at least 95% identity based on the Clustal alignment method.

5 21. The polypeptide of Claim 15, wherein the first amino acid sequence comprises the amino acid sequence of SEQ ID NO:10, wherein the second amino acid sequence comprises the amino acid sequence of SEQ ID NO:2, wherein the third amino acid sequence comprises the amino acid sequence of SEQ ID NO:4, wherein the fourth amino acid sequence comprises the amino acid sequence of SEQ ID NO:14, wherein the fifth amino acid sequence comprises the amino acid sequence of SEQ ID NO:12, wherein the sixth amino acid sequence comprises the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8, and wherein the seventh amino acid sequence comprises the amino acid sequence of SEQ ID NO:16.

10 22. The polypeptide of Claim 15, wherein the polypeptide is an aspartate kinase.

15 23. A method for transforming a cell comprising introducing the polynucleotide of any of Claims 1-9 into a cell.

20 24. A cell comprising the chimeric gene of Claim 10.

25. A method for producing a transgenic plant comprising transforming a plant cell with the polynucleotide of any of Claims 1-9 and regenerating a plant from the transformed plant cell.

26. A plant comprising the chimeric gene of Claim 10.

27. A seed comprising the chimeric gene of Claim 10.